



SEQUENCE LISTING

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STAZEWSKI, LENA
XU, HONG
EHEVERRI, FERNANDO

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<140> 09/897,427

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Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
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Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
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Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
          50          55          60

Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
 65          70          75          80

Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
          85          90          95

Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
          100          105          110

Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
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Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
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Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
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Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
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Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
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<210> 6

<211> 852

<212> PRT

<213> Homo sapiens

<400> 6

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Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
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Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
          20                      25                      30

```


Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser	340	345	350	
Ala	Leu	Gly	Glu	Arg	Glu	Gln	Gly	Leu	Glu	Glu	Asp	Val	Val	Gly	Gln	355	360	365	
Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly	370	375	380	
Leu	Asn	His	His	Gln	Thr	Phe	Ser	Val	Tyr	Ala	Ala	Val	Tyr	Ser	Val	385	390	395	400
Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	Cys	Asn	Ala	Ser	Gly	Cys	Pro	405	410	415	
Ala	Gln	Asp	Pro	Val	Lys	Pro	Trp	Gln	Leu	Leu	Glu	Asn	Met	Tyr	Asn	420	425	430	
Leu	Thr	Phe	His	Val	Gly	Gly	Leu	Pro	Leu	Arg	Phe	Asp	Ser	Ser	Gly	435	440	445	
Asn	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	Leu	Trp	Val	Trp	Gln	Gly	Ser	450	455	460	
Val	Pro	Arg	Leu	His	Asp	Val	Gly	Arg	Phe	Asn	Gly	Ser	Leu	Arg	Thr	465	470	475	480
Glu	Arg	Leu	Lys	Ile	Arg	Trp	His	Thr	Ser	Asp	Asn	Gln	Lys	Pro	Val	485	490	495	
Ser	Arg	Cys	Ser	Arg	Gln	Cys	Gln	Glu	Gly	Gln	Val	Arg	Arg	Val	Lys	500	505	510	
Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	Cys	Glu	Ala	Gly	Ser	515	520	525	
Tyr	Arg	Gln	Asn	Pro	Asp	Asp	Ile	Ala	Cys	Thr	Phe	Cys	Gly	Gln	Asp	530	535	540	
Glu	Trp	Ser	Pro	Glu	Arg	Ser	Thr	Arg	Cys	Phe	Arg	Arg	Arg	Ser	Arg	545	550	555	560
Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	565	570	575	
Ser	Leu	Ala	Leu	Gly	Leu	Val	Leu	Ala	Ala	Leu	Gly	Leu	Phe	Val	His	580	585	590	
His	Arg	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	Gly	Pro	Leu	Ala	Cys	595	600	605	
Phe	Gly	Leu	Val	Cys	Leu	Gly	Leu	Val	Cys	Leu	Ser	Val	Leu	Leu	Phe	610	615	620	
Pro	Gly	Gln	Pro	Ser	Pro	Ala	Arg	Cys	Leu	Ala	Gln	Gln	Pro	Leu	Ser	625	630	635	640

His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
 645 650 655
 Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
 660 665 670
 Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
 675 680 685
 Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
 690 695 700
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
 705 710 715 720
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
 725 730 735
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
 740 745 750
 Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
 755 760 765
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
 770 775 780
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
 785 790 795 800
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
 805 810 815
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
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 Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
 835 840 845
 Gly Lys His Glu
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<210> 7

<211> 2559

<212> DNA

<213> Homo sapiens

<400> 7

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<210> 8

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<220>

<221> MOD_RES

<222> (1)

<223> Thr or Arg

<220>

<221> MOD_RES

<222> (3)

<223> Phe or Leu

<220>

<221> MOD_RES

<222> (4)
 <223> Arg, Gln or Pro

<220>
 <221> MOD_RES
 <222> (6)
 <223> Arg or Thr

<220>
 <221> MOD_RES
 <222> (7)
 <223> Ser, Pro or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Val, Glu, Arg, Lys or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Ala or Glu

<220>
 <221> MOD_RES
 <222> (12)
 <223> Trp or Leu

<220>
 <221> MOD_RES
 <222> (13)
 <223> Arg, His or Gly

<400> 8
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<210> 9
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> Leu or Gln

<220>
 <221> MOD_RES
 <222> (3)
 <223> Glu, Gly or Thr

<220>
 <221> MOD_RES
 <222> (4)
 <223> Asn, Arg or Cys

<220>
 <221> MOD_RES
 <222> (7)
 <223> Arg or Glu

<220>
 <221> MOD_RES
 <222> (9)
 <223> Arg or Lys

<220>
 <221> MOD_RES
 <222> (10)
 <223> Cys, Gly or Phe

<220>
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 <222> (11)
 <223> Val, Leu or Ile

<220>
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 <222> (13)
 <223> Phe-or Leu

<220>
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 <222> (14)
 <223> Ala or Ser

<220>
 <221> MOD_RES
 <222> (15)
 <223> Met or Leu

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<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 10
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